IN THE CLAIMS:

In Claim 3, delete "or 2".

In Claim 5, delete "or 2".

Please amend Claim 6 as follows:

6. (amended) A peptide fragment [Peptide fragments] of the protein according to claim 1 [any one of claims 1 to 5] which results [which result] from the addition, deletion and/or replacement of one or more amino acids, said peptide fragment [fragments] having conserved the activity of interacting with the Vpu protein of HIV-1, the cell protein IκB or the cell protein β-catenin and/or with the skp1p protein.

7. (amemded) A nucleic acid sequence [Nucleic acid sequences] coding for the human protein h-bTrcp according to Claim 1 or a [and the] peptide fragment[s] that results from the addition, deletion and/or replacement of one or more amino acids, said peptide fragment having conserved the activity of interacting with the Vpu protein of HIV-1, the cell protein IκB or the cell protein β-catenin and/or with the skp1p protein, [according to any one of claims 1 to 6] characterized in that it consists [they consist] of:

a) the DNA sequence SEQ ID No. 1 or a [and the] DNA sequence[s] of the nucleic acid fragment[s] coding for said peptide fragment[s];

b) a DNA sequence which hybridizes [the DNA sequences which hybridize] under strict conditions with the above sequence[s] or [of] one of its fragments;

c) A DNA sequence [The DNA sequences] which, due to the degeneracy of the genetic code, results from the sequences a) and b) above and codes for the human protein h-βTrCP or fragments thereof; or [and]

d) a [the corresponding] mRNA and cDNA sequence[s] corresponding to a), b), or c).

Delete Claims 8 - 21 and substitute the following claims 37 - 50:

-- 37. A method of identifying anti-HIV-1 antiviral agents, the method comprising the step of screening anti-HIV antiviral agent candidates using the h-βTrCP protein of Claim 1, or a fragment thereof, to determine the capability of the anti-HIV antiviral agent candidates to inhibit the interaction between h-βTrCP protein and Vpu protein.

38. A method of identifying anti-HIV-1 antiviral agents, the method comprising the step of screening anti-HIV antiviral agent candidates using the h-βTrCP protein of Claim 1, or a fragment thereof, to determine the capability of the anti-HIV antiviral agent candidates to inhibit the interaction between h-βTrCP protein and Skp1p protein.

39. A method of identifying anti-HIV-1 antiviral agents, the method comprising the step of screening anti-HIV antiviral agent candidates using a nucleic acid sequence of Claim 7, or a fragment thereof, to determine the capability of the putative anti-HIV antiviral agent candidates to inhibit the interaction between h-βTrCP protein and Vpu protein.

40. A method of identifying anti-HIV-1 antiviral agents, the method comprising the step of screening anti-HIV antiviral agent candidates using a nucleic acid sequence of Claim 7, or a fragment thereof, to determine the capability of the anti-HIV antiviral agent candidates to inhibit the interaction between h-βTrCP protein and Skp1p protein.

41. A method of identifying antitumoral agents, the method comprising the step of screening antitumoral agent candidates using the h-βTrCP protein of Claim 1, or a fragment thereof, to determine the capability of the antitumoral agent candidates to perturb the regulation of the cell

cycle or protein degradation processes in tumoral human cells by modulating the interaction between h-βTrCP protein and Sdp1p protein.

42. A method of identifying antitumoral agents, the method comprising the step of screening antitumoral agent candidates using a nucleic acid sequence of Claim 7, or a fragment thereof, to determine the capability of the antitumoral agent candidates to perturb the regulation of the cell cycle or protein degradation processes in tumoral human cells by modulating the interaction between h-βTrCP protein and Sdp1p protein.

43. A method of identifying anti-inflammatory agents, the method comprising the step of screening anti-inflammatory agent candidates using the h-βTrCP protein of Claim 1, or a fragment thereof, to determine the capability of the anti-inflammatory agent candidates to perturb activation of the NFκB transcription factor by inhibiting the the interaction between h-βTrCP protein and the IκkB protein.

44. A method of identifying anti-inflammatory agents, the method comprising the step of screening anti-inflammatory agent candidates using a nucleic acid sequence of Claim 7, or a fragment thereof, to determine the capability of the anti-inflammatory agent candidates to perturb activation of the NFκB transcription factor by inhibiting the the interaction between h-βTrCP protein and the IκkB protein.

45. A method of identifying antitumoral agents, the method comprising the step of screening antitumoral agent candidates using the h-βTrCP protein of Claim 1, or a fragment thereof, to determine the capability of the antitumoral agent candidates to reactivate the interaction between h-βTrCP protein and a mutated β-catenin protein in tumoral cells, or between h-βTrCP protein and normal β-catenin in tumoral cells devoid of the APC protein.

46. A method of identifying antitumoral agents, the method comprising the step of screening antitumoral agent candidates using a nucleic acid sequence of Claim 7, or a fragment thereof, to determine the capability of the antitumoral agent candidates to reactivate the interaction between h-βTrCP protein and a mutated β-catenin protein in tumoral cells, or between h-βTrCP protein and normal β-catenin in tumoral cells devoid of the APC protein.

47. A method of identifying anti-Alzheimer agents, the method comprising the step of screening anti-Alzheimer agent candidates using the h-βTrCP protein of Claim 1, or a fragment thereof, to determine the capability of the anti-Alzheimer agent candidates to reduce the degree of degradation of β-catenin by inhibiting the interaction between h-βTrCP protein and the β-catenin protein.

48. A method of identifying anti-Alzheimer agents, the method comprising the step of screening anti-Alzheimer agent candidates using a nucleic acid sequence of Claim 7, or a fragment thereof, to determine the capability of the anti-Alzheimer agent candidates to reduce the degree of degradation of β-catenin by inhibiting the interaction between h-βTrCP protein and the β-catenin protein.

49. A method of detecting β-catenin mutations, the method comprising the step of carrying out a yeast two-hybrid screening with β-catenin derived from a sample and the h-βTrCP protein of Claim 1, or a fragment thereof.

50. A method of detecting β-catenin mutations, the method comprising the step of carrying out a yeast two-hybrid screening with β-catenin derived from a sample and a nucleic acid sequence of Claim 1, or a fragment thereof.--

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In Claim 24, delete "or the peptide fragments as defined in any one of claims 1 to 6" and insert --as defined in Claim 1 or peptide fragments thereof.--

In Claim 25, delete "or the peptide fragments as defined in any one of claims 1 to 6" and insert --as defined in Claim 1 or peptide fragments thereof.--

In Claim 25, delete "according to claim 7" and insert --coding for the human protein h-βTrcp or peptide fragments thereof.--

In Claim 29, delete "any one of claims 1 to 6" and insert --Claim 1--.

REMARKS

The specification has been amended to correct minor errors.

Claims 8 - 21 have been deleted and replaced by new claims 36 - 50 to convert the claims from non-statutory "use" claims to statutory process claims

The claims have been amended to avoid the inclusion of multiple dependent claims. In instances where doing so would introduce ambiguity into a claim, the claims have been amended accordingly.

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Applicants respectfully request entry of this amendment prior to calculation of the filing fee.

Respectfully submitted,

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